

SEQUENCE LISTING

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<120> Immunoglobulins

<130> PB60806

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<150> GB 0407197.3

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<150> GB 0407193.2

<151> 2004-03-30

<160> 65

<170> PatentIn version 3.1

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<213> Mus sp.

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<213> Mus sp.

<400> 3

Ser Pro Asn Ser Asn Phe Tyr Trp Tyr Phe Asp Val
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<213> Mus sp.

<400> 4

Ser Gly Ser Ser Ser Val Ser Tyr Met Tyr
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<213> Mus sp.

<400> 5

Asp Thr Ser Asn Leu Ala Ser
1 5

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<400> 6

Gln Gln Trp Ser Ser Tyr Pro Pro Thr
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<210> 7

<211> 120

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<213> Mus sp.

<400> 7

Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Arg Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Met
50 55 60

Ser Arg Leu Ser Ile Thr Lys Asp Asn Ser Arg Ser Gln Val Phe Phe
65 70 75 80

Lys Met Asn Ser Leu Gln Ala Asp Asp Thr Ala Ile Tyr Tyr Cys Ala
85 90 95

Lys Ser Pro Asn Ser Asn Phe Tyr Trp Tyr Phe Asp Val Trp Gly Thr
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 8

<211> 106

<212> PRT

<213> Mus sp.

<400> 8

Gln Ile Val Leu Thr Gln Ser Pro Thr Ile Met Ser Ala Ser Pro Gly
1 5 10 15

Glu Lys Val Thr Met Thr Cys Ser Gly Ser Ser Ser Val Ser Tyr Met
20 25 30

Tyr Trp Tyr Gln Glu Lys Pro Gly Ser Ser Pro Arg Leu Leu Ile Glu
35 40 45

Asp Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Pro Thr
85 90 95

Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 9

<211> 120

<212> PRT

<213> Artificial sequence

<220>

<223> VH domain (humanised, B3)

<400> 9

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Arg Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Met
50 55 60

Ser Arg Phe Thr Ile Ser Lys Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Lys Ser Pro Asn Ser Asn Phe Tyr Trp Tyr Phe Asp Val Trp Gly Arg
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 10

<211> 106

<212> PRT

<213> Artificial sequence

<220>

<223> VL domain (humanised, L2)

<400> 10

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Ser Gly Ser Ser Ser Val Ser Tyr Met
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Glu
35 40 45

Asp Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Asn Leu Glu Pro Glu
65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Pro Thr
85 90 95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 11

<211> 450

<212> PRT

<213> Artificial sequence

<220>

<223> Heavy chain (humanised)

<400> 11

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Arg Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Met
50 55 60

Ser Arg Phe Thr Ile Ser Lys Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Lys Ser Pro Asn Ser Asn Phe Tyr Trp Tyr Phe Asp Val Trp Gly Arg
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 12

<211> 213

<212> PRT

<213> Artificial sequence

<220>

<223> Light chain (humanised)

<400> 12

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Ser Gly Ser Ser Ser Val Ser Tyr Met
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Glu
35 40 45

Asp Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Asn Leu Glu Pro Glu
65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Pro Thr
85 90 95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys
210

<210> 13

<211> 252

<212> PRT

<213> Homo sapiens

<400> 13

Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
1 5 10 15

Leu Leu Phe Pro Ser Met Ala Ser Met Ala Ala Ile Gly Ser Cys Ser
20 25 30

Lys Glu Tyr Arg Val Leu Leu Gly Gln Leu Gln Lys Gln Thr Asp Leu
35 40 45

Met Gln Asp Thr Ser Arg Leu Leu Asp Pro Tyr Ile Arg Ile Gln Gly
50 55 60

Leu Asp Val Pro Lys Leu Arg Glu His Cys Arg Glu Arg Pro Gly Ala
65 70 75 80

Phe Pro Ser Glu Glu Thr Leu Arg Gly Leu Gly Arg Arg Gly Phe Leu
85 90 95

Gln Thr Leu Asn Ala Thr Leu Gly Cys Val Leu His Arg Leu Ala Asp
100 105 110

Leu Glu Gln Arg Leu Pro Lys Ala Gln Asp Leu Glu Arg Ser Gly Leu
115 120 125

Asn Ile Glu Asp Leu Glu Lys Leu Gln Met Ala Arg Pro Asn Ile Leu
130 135 140

Gly Leu Arg Asn Asn Ile Tyr Cys Met Ala Gln Leu Leu Asp Asn Ser
145 150 155 160

Asp Thr Ala Glu Pro Thr Lys Ala Gly Arg Gly Ala Ser Gln Pro Pro
165 170 175

Thr Pro Thr Pro Ala Ser Asp Ala Phe Gln Arg Lys Leu Glu Gly Cys
180 185 190

Arg Phe Leu His Gly Tyr His Arg Phe Met His Ser Val Gly Arg Val
195 200 205

Phe Ser Lys Trp Gly Glu Ser Pro Asn Arg Ser Arg Arg His Ser Pro
210 215 220

His Gln Ala Leu Arg Lys Gly Val Arg Arg Thr Arg Pro Ser Arg Lys
225 230 235 240

Gly Lys Arg Leu Met Thr Arg Gly Gln Leu Pro Arg
245 250

<210> 14

<211> 759

<212> DNA

<213> Homo sapiens

<400> 14
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cagctccaga agcagacaga tctcatgcag gacaccagca gactcctgga cccctatata 180
cgtatccaag gcctggatgt tcctaaactg agagagcact gcagggagcg ccccgggggc 240
ttccccagtg aggagaccct gagggggctg ggcaggcggg gcttcctgca gaccctcaat 300
gccacactgg gctgcgctct gcacagactg gccgacttag agcagcgctt cccaaggcc 360
caggatttgg agaggtctgg gctgaacatc gaggacttgg agaagctgca gatggcgagg 420
ccgaacatcc tcgggctcag gaacaacatc tactgcatgg ccagctgct ggacaactca 480
gacacggctg agcccacgaa ggctggccgg ggggcctctc agccgcccac cccaccct 540
gcctcggatg cttttcagcg caagctggag ggctgcaggt tcctgcatgg ctaccatcgc 600
ttcatgcact cagtggggcg ggtcttcagc aagtgggggg agagcccgaa ccggagccgg 660
agacacagcc cccaccaggc cctgaggaag ggggtgcgca ggaccagacc ctccaggaaa 720
ggcaagagac tcatgaccag gggacagctg ccccggtag 759

<210> 15

<211> 360

<212> DNA

<213> Mus sp.

<400> 15
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ccaggaaagg gtctggagtg gctgggagtg atatggagag gtggaagcac agactacaat 180
gcagctttca tgtccagact gagcatcacc aaggacaact ccaggagcca agttttcttt 240
aaaatgaaca gtctacaagc tgatgacact gccatatact actgtgcca aagtccgaat 300
agtaactttt actggtattt cgatgtctgg ggcacaggga ccacggtcac cgtctcctca 360

<210> 16

<211> 318

<212> DNA

<213> Mus sp.

<400> 16

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caaattgttc tcaccagtc tccaacaatc atgtctgcat ctccagggga gaaggtcacc      60
atgacctgca gtggcagctc aagtgttaagt tacatgtatt ggtaccagga gaagccagga    120
tcctcccca gactcctgat tgaagacaca tccaacctgg cttctggagt ccctgctcgc     180
ttcagtggca gtgggtctgg gacctcttac tctctcacia tcagccgaat ggaggctgaa    240
gatgctgcca cttattactg tcaacagtgg agtagttatc caccacggtt cggctcgggg    300
acaaagttgg aaatcaaa                                     318
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<210> 17

<211> 360

<212> DNA

<213> Artificial sequence

<220>

<223> VH domain (humanised, PN, B3)

<400> 17

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tcctgtgcag cgtctggatt ctcattaact aattatggtg tacactgggt cgcaggct      120
ccaggcaagg ggctggagtg ggtggcagtg atatggagag gtggaagcac agactacaat     180
gcagctttca tgtcccgatt caccatctcc aaggacaatt ccaagaacac gctgtatctg    240
caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgaa aagtccgaat    300
agtaactttt actggtattt cgatgtcttg ggccgtggca cactagtcac agtctcctca    360
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<210> 18

<211> 318

<212> DNA

<213> Artificial sequence

<220>

<223> VL domain (humanised, PN, L2)

<400> 18

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gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc      60
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caggctccca ggctcctcat cgaagacaca tccaacctgg cttctggcat cccagccagg      180
ttcagtggca gtgggtctgg gacagactac actctcacca tcagcaacct agagcctgaa      240
gattttgcag tttattactg tcaacagtgg agtagttatc caccacggtt tggccagggg      300
accaagctgg agatcaaa                                     318
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<210> 19

<211> 1350

<212> DNA

<213> Artificial sequence

<220>

<223> Heavy chain (humanised, PN)

<400> 19

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tcctgtgcag cgtctggatt ctcattaact aattatggtg tacactgggt cgcagggt      120
ccaggcaagg ggctggagtg ggtggcagtg atatggagag gtggaagcac agactacaat      180
gcagctttca tgtcccgatt caccatctcc aaggacaatt ccaagaacac gctgtatctg      240
caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgaa aagtccgaat      300
agtaactttt actggtattht cgatgtcttg ggccgtggca cactagtcac agtctcctca      360
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg      420
ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg      480
tggaactcag gcgccctgac cagcggcgctg cacaccttcc cggctgtcct acagtccctca      540
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc      600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc      660
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aaatcttgtg	acaaaactca	acatgcca	ccgtgcccag	cacctgaact	cctgggggga	720
ccgtcagtct	tcctcttccc	cccaaaaccc	aaggacaccc	tcatgatctc	ccggaccct	780
gaggtcacat	gcgtgggtgt	ggacgtgagc	cacgaagacc	ctgaggtcaa	gttcaactgg	840
tacgtggacg	gcgtggaggt	gcataatgcc	aagacaaagc	cgcgaggagga	gcagtacaac	900
agcacgtacc	gtgtgggtcag	cgtcctcacc	gtcctgcacc	aggactggct	gaatggcaag	960
gagtacaagt	gcaaggtctc	caacaaagcc	ctcccagccc	ccatcgagaa	aaccatctcc	1020
aaagccaaag	ggcagccccg	agaaccacag	gtgtacaccc	tgcccccatc	ccgggatgag	1080
ctgaccaaga	accaggtcag	cctgacctgc	ctgggtcaaag	gcttctatcc	cagcgacatc	1140
gccgtggagt	gggagagcaa	tgggcagccg	gagaacaact	acaagaccac	gcctcccgtg	1200
ctggactccg	acggctcctt	cttcctctac	agcaagctca	ccgtggacaa	gagcaggtgg	1260
cagcagggga	acgtcttctc	atgctccgtg	atgcatgagg	ctctgcacaa	ccactacacg	1320
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<210> 20

<211> 639

<212> DNA

<213> Artificial sequence

<220>

<223> Light chain (humanised, PN)

<400> 20

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ctctcctgca	gtggcagctc	aagtgttaagt	tacatgtatt	ggtaccaaca	gaaacctggc	120
caggctccca	ggctcctcat	cgaagacaca	tccaacctgg	cttctggcat	cccagccagg	180
ttcagtggca	gtgggtcttg	gacagactac	actctcacca	tcagcaacct	agagcctgaa	240
gattttgcag	tttattactg	tcaacagtgg	agtagttatc	caccacagtt	tggccagggg	300
accaagctgg	agatcaaacg	tacgggtggct	gcaccatctg	tcttcatctt	cccgccatct	360
gatgagcagt	tgaaatctgg	aactgcctct	gttgtgtgcc	tgctgaataa	cttctatccc	420
agagaggcca	aagtacagtg	gaaggtggac	aacgccctcc	aatcgggtaa	ctcccaggag	480

agtgtcacag agcaggacag caaggacagc acctacagcc tcagcagcac cctgacgctg 540
 agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcaccca tcagggcctg 600
 agctcgccccg tcacaaagag cttcaacagg ggagagtgt 639

<210> 21

<211> 120

<212> PRT

<213> Artificial sequence

<220>

<223> VH domain (B4, humanised)

<400> 21

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Leu Thr Asn Tyr
 20 25 30

Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Val Ile Trp Arg Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Met
 50 55 60

Ser Arg Leu Thr Ile Ser Lys Asp Asn Ser Lys Asn Thr Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Lys Ser Pro Asn Ser Asn Phe Tyr Trp Tyr Phe Asp Val Trp Gly Arg
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 22

<211> 37

<212> DNA

<213> Artificial sequence

<220>

<223> VH forward primer

<400> 22

gatgaagctt gccaccatgg ctgtcctagg gctactc

37

<210> 23

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<223> VH reverse primer

<400> 23

gatggactag tgtccctgtg ccccagac

28

<210> 24

<211> 37

<212> DNA

<213> Artificial sequence

<220>

<223> VL forward primer

<400> 24

gatgaagctt gccaccatgg attttcaggt gcagatt

37

<210> 25

<211> 31

<212> DNA

<213> Artificial sequence

<220>

<223> VL reverse primer

<400> 25

gatgcgtacg tttgatttcc aactttgtcc c

31

<210> 26

<211> 124

<212> PRT

<213> Homo sapiens

<400> 26

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Ser Pro Ser Ser Gly Ser Tyr Tyr Tyr Tyr Tyr Tyr Gly Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 27

<211> 121

<212> PRT

<213> Homo sapiens

<400> 27

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Leu Gly Gly Pro Leu Tyr Trp Tyr Phe Asp Leu Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 28

<211> 106

<212> PRT

<213> Homo sapiens

<400> 28

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Lys Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
100 105

<210> 29

<211> 116

<212> PRT

<213> Artificial sequence

<220>

<223> Humanised VH construct A1

<400> 29

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Val Ile Trp Arg Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Met
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Val Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Lys Ser Pro Asn Ser Asn Phe Tyr Trp Tyr Phe Asp Val Trp Gly Gln
100 105 110

Gly Thr Thr Ser
115

<210> 30

<211> 116

<212> PRT

<213> Artificial sequence

<220>

<223> Humanised VH construct A2

<400> 30

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Val Ile Trp Arg Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Met
50 55 60

Ser Arg Val Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Lys Ser Pro Asn Ser Asn Phe Tyr Trp Tyr Phe Asp Val Trp Gly Gln
100 105 110

Gly Thr Thr Ser
115

<210> 31

<211> 116

<212> PRT

<213> Artificial sequence

<220>

<223> Humanised VH construct A3

<400> 31

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Val Ile Trp Arg Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Met
50 55 60

Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Asn Gln Val Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Lys Ser Pro Asn Ser Asn Phe Tyr Trp Tyr Phe Asp Val Trp Gly Gln
100 105 110

Gly Thr Thr Ser
115

<210> 32

<211> 116

<212> PRT

<213> Artificial sequence

<220>

<223> Humanised VH construct A4

<400> 32

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Val Ile Trp Arg Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Met
50 55 60

Ser Arg Leu Thr Ile Ser Lys Asp Asn Ser Lys Asn Gln Val Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Lys Ser Pro Asn Ser Asn Phe Tyr Trp Tyr Phe Asp Val Trp Gly Gln
100 105 110

Gly Thr Thr Ser
115

<210> 33

<211> 116

<212> PRT

<213> Artificial sequence

<220>

<223> Humanised VH construct B1

<400> 33

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Arg Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Met
50 55 60

Ser Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Ser Pro Asn Ser Asn Phe Tyr Trp Tyr Phe Asp Val Trp Gly Arg
100 105 110

Gly Thr Leu Val
115

<210> 34

<211> 116

<212> PRT

<213> Artificial sequence

<220>

<223> Humanised VH construct B2

<400> 34

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Arg Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Met
50 55 60

Ser Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Lys Ser Pro Asn Ser Asn Phe Tyr Trp Tyr Phe Asp Val Trp Gly Arg
100 105 110

Gly Thr Leu Val
115

<210> 35

<211> 116

<212> PRT

<213> Artificial sequence

<220>

<223> Humanised VH construct B3

<400> 35

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Arg Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Met
50 55 60

Ser Arg Phe Thr Ile Ser Lys Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Lys Ser Pro Asn Ser Asn Phe Tyr Trp Tyr Phe Asp Val Trp Gly Arg
100 105 110

Gly Thr Leu Val
115

<210> 36

<211> 116

<212> PRT

<213> Artificial sequence

<220>

<223> Humanised VH construct B4

<400> 36

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Arg Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Met
50 55 60

Ser Arg Leu Thr Ile Ser Lys Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Lys Ser Pro Asn Ser Asn Phe Tyr Trp Tyr Phe Asp Val Trp Gly Arg
100 105 110

Gly Thr Leu Val
115

<210> 37

<211> 106

<212> PRT

<213> Artificial sequence

<220>

<223> Humanised VL construct L1

<400> 37

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Ser Gly Ser Ser Ser Val Ser Tyr Met
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
35 40 45

Asp Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Glu Pro Glu
65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Pro Thr
85 90 95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 38

<211> 106

<212> PRT

<213> Artificial sequence

<220>

<223> Humanised VL construct L2

<400> 38

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Ser Gly Ser Ser Ser Val Ser Tyr Met
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Glu
35 40 45

Asp Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Asn Leu Glu Pro Glu
65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Pro Thr
85 90 95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 39

<211> 19

<212> PRT

<213> Homo sapiens

<400> 39

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
1				5					10					15	

Val His Ser

<210> 40

<211> 5

<212> PRT

<213> Mus sp.

<400> 40

Asp	Tyr	Asn	Met	Asp
1				5

<210> 41

<211> 17

<212> PRT

<213> Mus sp.

<400> 41

Asp	Ile	Asn	Pro	Asn	Asn	Gly	Gly	Thr	Ile	Asp	Asn	Gln	Lys	Phe	Lys
1				5					10					15	

Asp

<210> 42

<211> 12

<212> PRT

<213> Mus sp.

<400> 42

Gly	Ile	Tyr	Tyr	Tyr	Gly	Ser	His	Tyr	Phe	Asp	Tyr
1				5					10		

<210> 43

<211> 10

<212> PRT

<213> Mus sp.

<400> 43

Ser	Ala	Thr	Ser	Ser	Val	Ser	Val	Met	His
1				5					10

<210> 44

<211> 7

<212> PRT

<213> Mus sp.

<400> 44

Asp	Thr	Ser	Lys	Leu	Ala	Ser
1				5		

<210> 45

<211> 9

<212> PRT

<213> Mus sp.

<400> 45

Gln Gln Trp Ser Ser Asn Pro Leu Thr
1 5

<210> 46

<211> 121

<212> PRT

<213> Mus sp.

<400> 46

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Asp Tyr
20 25 30

Asn Met Asp Trp Val Lys Gln Ser His Gly Lys Lys Leu Glu Trp Ile
35 40 45

Gly Asp Ile Asn Pro Asn Asn Gly Gly Thr Ile Asp Asn Gln Lys Phe
50 55 60

Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Ile Tyr Tyr Tyr Gly Ser His Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Leu Thr Val Ser Ser
115 120

<210> 47

<211> 106

<212> PRT

<213> Mus sp.

<400> 47

Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
1 5 10 15

Glu Lys Val Thr Met Thr Cys Ser Ala Thr Ser Ser Val Ser Val Met
20 25 30

His Trp Phe Gln Lys Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Thr Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65 70 75 80

Asp Thr Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Ser Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 48

<211> 121

<212> PRT

<213> Artificial sequence

<220>

<223> VH domain (humanised, B3)

<400> 48

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Asp Tyr
20 25 30

Asn Met Asp Trp Val Arg Gln Ala Pro Gly Gln Lys Leu Glu Trp Ile
35 40 45

Gly Asp Ile Asn Pro Asn Asn Gly Gly Thr Ile Asp Asn Gln Lys Phe
50 55 60

Lys Asp Arg Ala Thr Leu Thr Val Asp Lys Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Ile Tyr Tyr Tyr Gly Ser His Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 49

<211> 106

<212> PRT

<213> Artificial sequence

<220>

<223> VL domain (humanised, L2)

<400> 49

Glu Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Thr Ser Ser Val Ser Val Met
20 25 30

His Trp Phe Gln Lys Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
65 70 75 80

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Asp Ile Lys
100 105

<210> 50

<211> 451

<212> PRT

<213> Artificial sequence

<220>

<223> Heavy chain (humanised)

<400> 50

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Asp Tyr
20 25 30

Asn Met Asp Trp Val Arg Gln Ala Pro Gly Gln Lys Leu Glu Trp Ile
35 40 45

Gly Asp Ile Asn Pro Asn Asn Gly Gly Thr Ile Asp Asn Gln Lys Phe
50 55 60

Lys Asp Arg Ala Thr Leu Thr Val Asp Lys Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Ile Tyr Tyr Tyr Gly Ser His Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 51

<211> 213

<212> PRT

<213> Artificial sequence

<220>

<223> Light chain (humanised)

<400> 51

Glu Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Thr Ser Ser Val Ser Val Met
20 25 30

His Trp Phe Gln Lys Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
65 70 75 80

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys
210

<210> 52

<211> 363

<212> DNA

<213> Mus sp.

<400> 52

gaggtccagc	tgcaacagtc	tggaacctgag	ctggtgaagc	ctgggggcttc	agtgaagata	60
tcctgcaagg	cctctggata	catattcact	gactacaaca	tggaactgggt	gaagcagagc	120
catggaaaga	aacttgagtg	gattggagat	attaatccta	ataatgggtg	tactatcgac	180
aaccagaagt	tcaaggacaa	ggccacattg	actgtagaca	agtcctccag	cacagcctac	240
atggagctcc	gcagcctgac	atctgaggac	actgcagtct	attactgtgc	aagagggatt	300
tattactacg	gtagtcacta	ctttgactat	tggggccaag	gcaccactct	cacagtctcc	360
tca						363

<210> 53

<211> 318

<212> DNA

<213> Mus sp.

<400> 53

caaattgttc	tcacccagtc	tccagcaatc	atgtctgcat	ctccagggga	gaaggtcacc	60
atgacctgca	gtgccacctc	aagtgtgaagt	gtcatgcact	ggttccagaa	gaagtcaggt	120
acctccccca	aaagatggat	ttatgacaca	tccaaactgg	cttctggagt	ccctactcgc	180
ttcagtggca	gtgggtctgg	gacctcttac	tctctcacia	tcagtagcat	ggaggctgaa	240
gatactgcca	cttattactg	ccagcagtg	agtagtaacc	cactcacgtt	cggttctggg	300
accaagctgg	agctgaaa					318

<210> 54

<211> 363

<212> DNA

<213> Artificial sequence

<220>

<223> VH domain (humanised, PN, B3)

<400> 54

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gaggtccagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt      60
tcctgcaagg catctggata catattcacc gactacaaca tggactgggt gcgacaggcc      120
cctggacaaa aacttgagtg gattggagat attaatccta ataatggtgg tactatcgac      180
aaccagaagt tcaaggacag agccaccttg accgtagaca agtccacgag cacagtctac      240
atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagagggatt      300
tattactacg gtagtcacta ctttgactat tggggccagg gaacactagt cacagtctcc      360
tca                                                                    363
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<210> 55

<211> 318

<212> DNA

<213> Artificial sequence

<220>

<223> VL domain (humanised, PN, L2)

<400> 55

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gaaattgtgt tgacgcagtc tccatcctcc ctgtctgcat ctgttgagaa cagagtcacc      60
atcacttgca gtgccacctc aagtgtgaagt gtcatgcact ggttccagaa gaaaccaggg      120
aaagccccta agagatggat ctatgacaca tccaaactgg cttctgggggt cccatcaagg      180
ttcagtggca gtggatctgg gacagattac actctcacca tcagcagtct gcaacctgaa      240
gattttgcaa cttattactg ccagcagtgg agtagtaacc cactcacgtt cggcggaggg      300
accaaagtgg atatcaaa                                                                    318
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<210> 56

<211> 1353

<212> DNA

<213> Artificial sequence

<220>

<223> Heavy chain (humanised, PN)

<400> 56

gaggtccagc	tgggtgcagtc	tggggctgag	gtgaagaagc	ctggggcctc	agtgaaggtt	60
tcctgcaagg	catctggata	catattcacc	gactacaaca	tggactgggt	gcgacaggcc	120
cctggacaaa	aacttgagtg	gattggagat	attaatccta	ataatgggtg	tactatcgac	180
aaccagaagt	tcaaggacag	agccaccttg	accgtagaca	agtccacgag	cacagtctac	240
atggagctga	gcagcctgag	atctgaggac	acggccgtgt	attactgtgc	gagagggatt	300
tattactacg	gtagtcacta	ctttgactat	tggggccagg	gaacactagt	cacagtctcc	360
tcagcctcca	ccaagggccc	atcgggtcttc	cccctggcac	cctcctccaa	gagcacctct	420
gggggacacag	cggccctggg	ctgcctggtc	aaggactact	tccccgaacc	ggtgacggtg	480
tcgtggaact	caggcgccct	gaccagcggc	gtgcacacct	tcccggctgt	cctacagtcc	540
tcaggactct	actccctcag	cagcgtgggtg	accgtgccct	ccagcagctt	gggcacccag	600
acctacatct	gcaacgtgaa	tcacaagccc	agcaacacca	aggtggacaa	gaaagttgag	660
cccaaattctt	gtgacaaaac	tcacacatgc	ccaccgtgcc	cagcacctga	actcctgggg	720
ggaccgtcag	tcttcctctt	ccccccaaaa	cccaaggaca	ccctcatgat	ctcccggacc	780
cctgaggtca	catgcgtggg	ggtggacgtg	agccacgaag	accctgaggt	caagttcaac	840
tggtagctgg	acggcgtgga	ggtgcataat	gccaaagacaa	agccgcggga	ggagcagtac	900
aacagcacgt	accgtgtggg	cagcgtcctc	accgtcctgc	accaggactg	gctgaatggc	960
aaggagtaca	agtgaagggt	ctccaacaaa	gccctcccag	cccccatcga	gaaaaccatc	1020
tccaaagcca	aagggcagcc	ccgagaacca	caggtgtaca	ccctgcccc	atcccgggat	1080
gagctgacca	agaaccaggt	cagcctgacc	tgcttggtca	aaggcttcta	tcccagcgac	1140
atcgccgtgg	agtgggagag	caatgggcag	ccggagaaca	actacaagac	cacgcctccc	1200
gtgctggact	ccgacggctc	cttcttcttc	tacagcaagc	tcaccgtgga	caagagcagg	1260
tggcagcagg	ggaacgtctt	ctcatgctcc	gtgatgcatg	aggctctgca	caaccactac	1320
acgcagaaga	gcctctccct	gtctccgggt	aaa			1353

<210> 57

<211> 639

<212> DNA

<213> Artificial sequence

<220>

<223> Light chain (humanised, PN)

<400> 57

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gaaattgtgt tgacgcagtc tccatcctcc ctgtctgcat ctggttgaga cagagtcacc      60
atcacttgca gtgccacctc aagtgtgaagt gtcatgcact gggtccagaa gaaaccaggg      120
aaagccccta agagatggat ctatgacaca tccaaactgg cttctggggg cccatcaagg      180
ttcagtggca gtggatctgg gacagattac actctcacca tcagcagtct gcaacctgaa      240
gattttgcaa cttattactg ccagcagtgg agtagtaacc cactcacgtt cggcggaggg      300
accaaagtgg atatcaaacg tacggtggct gcaccatctg tcttcatctt cccgccatct      360
gatgagcagt tgaaatctgg aactgcctct gttgtgtgcc tgctgaataa cttctatccc      420
agagaggcca agtacagtg gaaggtggac aacgccctcc aatcgggtaa ctcccaggag      480
agtgtcacag agcaggacag caaggacagc acctacagcc tcagcagcac cctgacgctg      540
agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcaccca tcagggcctg      600
agctcgcccc tcacaaagag cttcaacagg ggagagtgt                                639
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<210> 58

<211> 37

<212> DNA

<213> Artificial sequence

<220>

<223> VH forward primer

<400> 58

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gatgaagctt gccaccatgg gatggagctg ggtcttt                                37
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<210> 59

<211> 37

<212> DNA

<213> Artificial sequence

<220>

<223> VL forward primer

<400> 59

gatgaagctt gccaccatgg atttacaggt gcagatt

37

<210> 60

<211> 31

<212> DNA

<213> Artificial sequence

<220>

<223> VL reverse primer

<400> 60

gatgcgtacg tttcagctcc agcttggtcc c

31

<210> 61

<211> 450

<212> PRT

<213> Artificial sequence

<220>

<223> Heavy chain (humanised, Fc mutated)

<400> 61

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Arg Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Met
50 55 60

Ser Arg Phe Thr Ile Ser Lys Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Lys Ser Pro Asn Ser Asn Phe Tyr Trp Tyr Phe Asp Val Trp Gly Arg
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Ala Gly Ala
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<211> 1350

<212> DNA

<213> Artificial sequence

<220>

<223> Heavy chain (humanised, Fc mutated, PN)

<400> 62

caggtgcagc	tggtggagtc	tgggggaggc	gtggtccagc	ctgggaggtc	cctgagactc	60
tcctgtgcag	cgtctggatt	ctcattaact	aattatggtg	tacactgggt	ccgccaggct	120
ccaggcaagg	ggctggagtg	ggtggcagtg	atatggagag	gtggaagcac	agactacaat	180
gcagctttca	tgtcccgatt	caccatctcc	aaggacaatt	ccaagaacac	gctgtatctg	240
caaatgaaca	gcctgagagc	cgaggacacg	gctgtgtatt	actgtgcgaa	aagtccgaat	300
agtaactttt	actggtatth	cgatgtcttg	ggccgtggca	cactagtcac	agtctcctca	360
gcctccacca	agggcccatc	ggtcttcccc	ctggcaccct	cctccaagag	cacctctggg	420
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Lys	Glu	Tyr	Arg	Met	Leu	Leu	Gly	Gln	Leu	Gln	Lys	Gln	Thr	Asp	Leu
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Met	Gln	Asp	Thr	Ser	Arg	Leu	Leu	Asp	Pro	Tyr	Ile	Arg	Ile	Gln	Gly
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Phe	Pro	Ser	Glu	Glu	Thr	Leu	Arg	Gly	Leu	Gly	Arg	Arg	Gly	Phe	Leu
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Gln	Thr	Leu	Asn	Ala	Thr	Leu	Gly	Cys	Val	Leu	His	Arg	Leu	Ala	Asp
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Leu	Glu	Gln	His	Leu	Pro	Lys	Ala	Gln	Asp	Leu	Glu	Arg	Ser	Gly	Leu
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Asn	Ile	Glu	Asp	Leu	Glu	Lys	Leu	Gln	Met	Ala	Arg	Pro	Asn	Val	Leu
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Gly	Leu	Arg	Asn	Asn	Val	Tyr	Cys	Met	Ala	Gln	Leu	Leu	Asp	Asn	Ser
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Asp Met Thr Glu Pro Thr Lys Ala Gly Arg Gly Thr Pro Gln Pro Pro
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Thr Pro Thr Pro Thr Ser Asp Val Phe Gln Arg Lys Leu Glu Gly Cys
180 185 190

Ser Phe Leu Arg Gly Tyr His Arg Phe Met His Ser Val Gly Arg Ile
195 200 205

Phe Ser Lys Trp Gly Glu Ser Pro Asn Arg Ser Arg Arg His Ser Pro
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